Supplementary material: Modelling results

High seroprevalence against Zika virus in Salvador, north-eastern Brazil limits the potential for further outbreaks

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Introduction

This document contains the R code necessary to reproduce the modelling results in “High seroprevalence against Zika virus in Salvador, north-eastern Brazil limits the potential for further outbreaks”.

Required packages

Install required packages

```r
cran_packages <- c("magrittr", "cowplot", "scales", "dplyr")
github_packages <- c("sbfnk/RBi.helpers")
```

```r
for (package in cran_packages) {
    install.packages(package)
}

library("devtools")

for (package in github_packages) {
    install_github(package)
}
```

Load required packages

```r
for (package in c(cran_packages, github_packages)) {
    library(tolower(sub("^.*/", "", package)), character.only = TRUE)
}
```

Model fitting

Generate posterior samples

Set the number of samples in the serological study

```
n_serology = 633
```

Read observations and model

```
model_dir <- path.expand("~/code/vbd/bi")
obs <- readRDS("fit_data.rds")
vbd_model <- bi_model(paste(model_dir, "vbd.bi", sep = "/"))
```

Set population size, initial population immune, and proportion of the population at risk to constants

```
vbd_model %<>% fix(N = 2675000, p_p_immune = 0.06, p_p_risk = 1)
```

Print data

```
obs
```

```
## $Incidence
## # A tibble: 43 x 2
##      time value
##     <int> <dbl>
##  1      1     9
##  2      2     6
##  3      3     8
##  4      4     9
##  5      5    18
##  6      6    17
##  7      7     7
##  8      8    15
##  9     9    14
## 10    10    10
## 11    11    43
## 12    12   107
## 13    13   147
## 14    14   161
## 15    15   298
## 16    16   440
## 17    17   408
## 18    18   706
## 19    19   777
## 20    20  1020
## 21    21  1033
## 22    22  1143
## 23    23  1100
## 24    24  1272
## 25    25  1265
## 26    26  1595
## 27    27  2371
## 28    28  2886
## 29    29  2470
## 30    30  1962
## 31    31  1603
## 32    32  1159
## 33    33   887
## 34    34   681
## 35    35   512
## 36    36   495
## 37    37   388
## 38    38   366
## 39    39   350
## 40    40   246
## 41    41   226
## 42    42   288
## 43    43   265
## 
## $Serology
##   time value
## 1   66   401
```

Print model

```
vbd_model
```

```
## bi_model:
## =========
##  1: model vbd {
##  2:   const p_p_risk = 1
##  3:   const p_p_immune = 0.06
##  4:   const N = 2675000
##  5:   param p_d_inc_h
##  6:   param p_d_inf_h
##  7:   param p_R0
##  8:   param p_p_rep
##  9:   param p_p_over
## 10:   param p_s_peak
## 11:   param p_s_amp
## 12:   param initI
## 13:   state S (has_output = 0)
## 14:   state E (has_output = 0)
## 15:   state I (has_output = 0)
## 16:   state R (has_output = 0)
## 17:   state Z (has_output = 0)
## 18:   state beta_track
## 19:   state Reff
## 20:   input serology_sample
## 21:   obs Incidence
## 22:   obs Serology
## 23:   sub parameter {
## 24:     p_d_inc_h ~ truncated_gaussian(mean = 17.8/7, std = 2.3/7, lower = 0)
## 25:     p_d_inf_h ~ truncated_gaussian(mean = 4.7/7, std = 1.2/7, lower = 0)
## 26:     p_R0 ~ uniform(lower = 0, upper = 25)
## 27:     p_s_amp ~ uniform(lower = 0, upper = 1)
## 28:     p_s_peak ~ gaussian(mean = 20, std = 2)
## 29:     p_p_rep ~ uniform(lower = 0, upper = 1)
## 30:     initI ~ gamma(shape = 1, scale = 10)
## 31:     p_p_over ~ beta(1, 10)
## 32:   }
## 33:   sub initial {
## 34:     S <- max(N * (1 - p_p_immune) * p_p_risk - initI, 0)
## 35:     E <- 0
## 36:     I <- initI
## 37:     R <- N * p_p_immune * p_p_risk
## 38:     Z <- 0
## 39:     beta_track <- p_R0/p_d_inf_h * (1 + p_s_amp*cos(6.283*(-p_s_peak)/52))
## 40:     Reff <- p_R0 * S / (N * p_p_risk) * (1 + p_s_amp*cos(6.283*(-p_s_peak)/52))
## 41:   }
## 42:   sub transition {
## 43:     inline incubation_rate = 1/p_d_inc_h
## 44:     inline recovery_rate = 1/p_d_inf_h
## 45:     inline infection_rate = p_R0/p_d_inf_h
## 46:     inline transmission_rate = infection_rate*(1+p_s_amp*cos(6.283*(t_now-p_s_peak)/52))
## 47:     beta_track <- transmission_rate
## 48:     Reff <- transmission_rate/recovery_rate * S/(N * p_p_risk)
## 49:     Z <- 0
## 50:     ode {
## 51:       dS/dt = -transmission_rate*S*I/(N*p_p_risk)
## 52:       dE/dt = +transmission_rate*S*I/(N*p_p_risk)-incubation_rate*E
## 53:       dI/dt = +incubation_rate*E-recovery_rate*I
## 54:       dR/dt = +recovery_rate*I
## 55:       dZ/dt = +incubation_rate*E
## 56:     }
## 57:   }
## 58:   sub observation {
## 59:     Incidence ~ truncated_gaussian(mean = p_p_rep * max(0, Z), std = sqrt(p_p_rep * max(
0, Z) / (1 - p_p_over)), lower=0)
## 60:     Serology ~ binomial(size = serology_sample, prob = R / (N * p_p_risk))
## 61:   }
## 62: }
```

Generate `libbi` object

```
bi <- libbi(vbd_model, input = list(serology_sample = n_serology), obs = obs,
    end_time = max(obs$Sero$time))
```

Generate prior samples (for plotting later)

```
bi_prior <- sample(bi, target = "prior", nsamples = 5000)
save_libbi(bi_prior, "salvador_prior.rds")
```

Generate and save posterior samples (after adapting the posterior distribution)

```
bi %<>% optimise() %>% sample(proposal = "prior", nsamples = 5000) %>% adapt_proposal(min = 0.1
,
    max = 0.4) %>% sample(sample_obs = TRUE, nsamples = 5e+05, thin = 50)
save_libbi(bi, "salvador.rds")
```

Prediction

Use the posterior samples to predict up to week 80

```
pred <- predict(bi, end_time = 80, noutputs = 80, sample_obs = TRUE)
save_libbi(pred, "salvador_prediction.rds")
```

\(R_0\) calculations

Calculate \(R_0\) at the beginning of the outbreak

```
res <- bi_read(pred)
R0_calc <- copy(res[c("beta_track", "p_d_inf_h")])
R0_calc <- lapply(names(R0_calc), function(x) {
    setnames(R0_calc[[x]], "value", x)
})
R0_df <- data.table(merge(R0_calc[[1]], R0_calc[[2]]))
R0_df <- R0_df[time == 0]
R0_df <- R0_df[, `:=`(value, beta_track * p_d_inf_h)]
```

Summary statistics of \(R_0\) and the reporting rate.

```
mean(R0_df$value)
```

```
## [1] 2.137214
```

```
quantile(R0_df$value, c(0.025, 0.975))
```

```
##     2.5%    97.5% 
## 1.787868 2.597923
```

```
mean(res$p_p_rep$value)
```

```
## [1] 0.01990676
```

```
quantile(res$p_p_rep$value, c(0.025, 0.975))
```

```
##       2.5%      97.5% 
## 0.01761499 0.02249363
```

Plots

Predictions

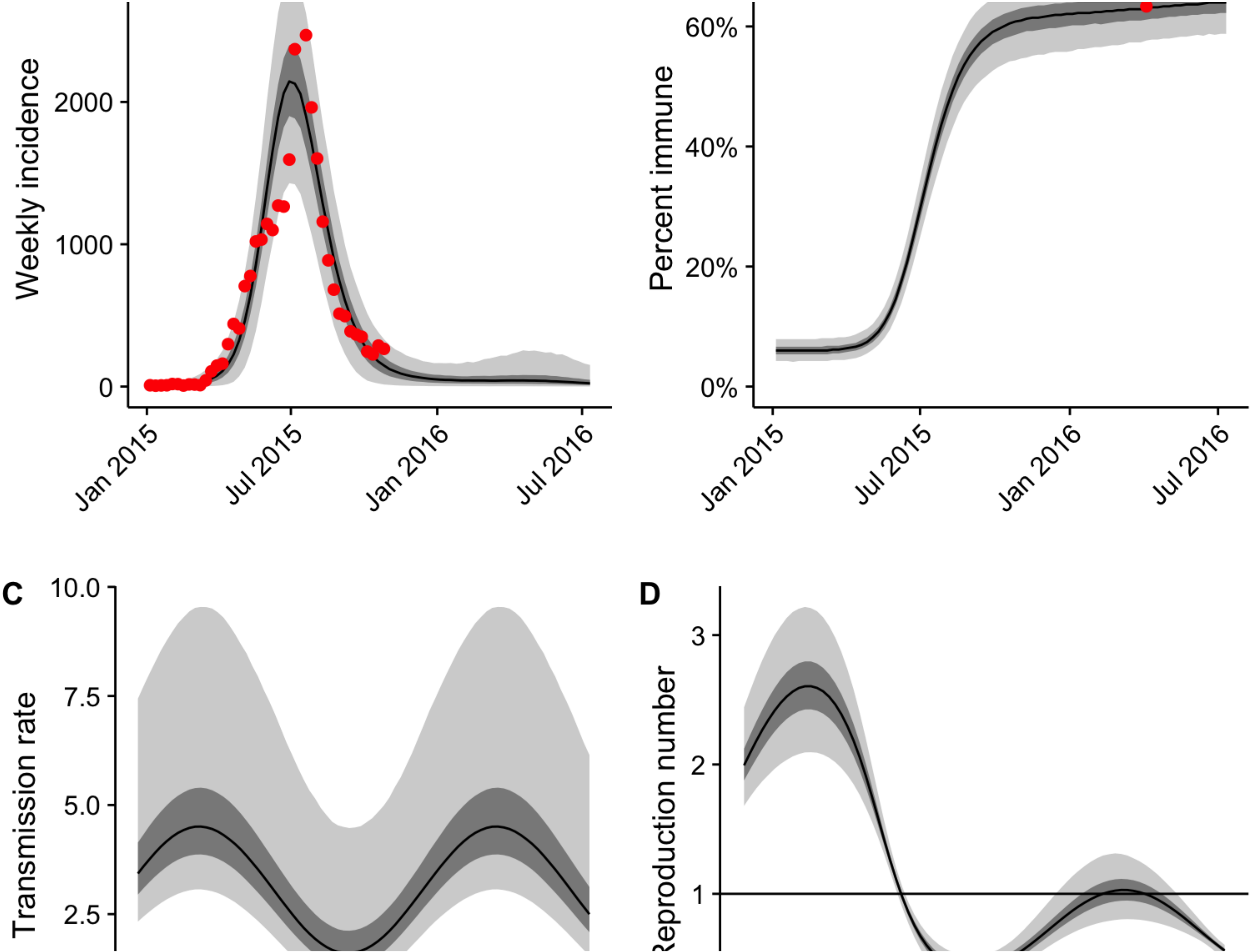
Express serology as proportion immune (in results and) data

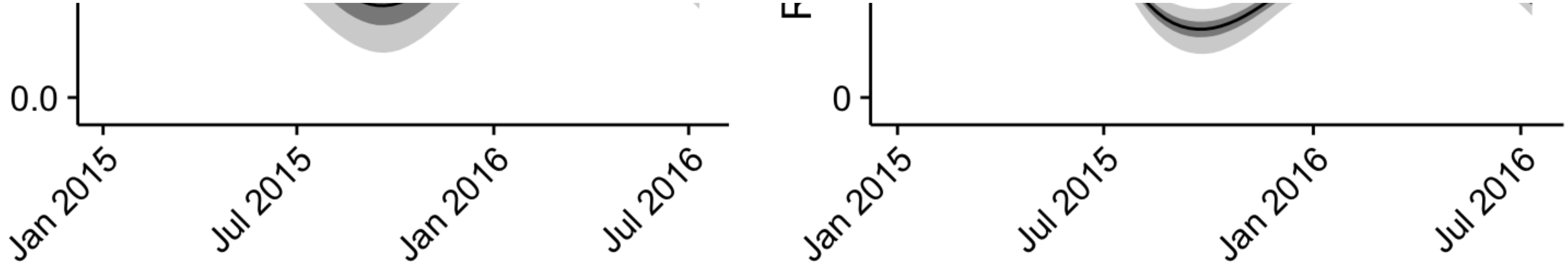
```
res$Serology %<>% mutate(value = value/n_serology)
pred %<>% attach_file(file = "output", data = res, force = TRUE)
```

```
pred_obs <- bi_read(pred, file = "obs")
pred_obs$Serology %<>% mutate(value = value/n_serology)
pred %<>% attach_file(file = "obs", data = pred_obs, force = TRUE)
```

Plot

```
common_plot_options <- list(x = pred, plot = FALSE, all.times = TRUE, select = list(time = 1:10
4),
    hline = c(Reff = 1), labels = c(beta_track = "beta", Reff = "R[eff]"), date.origin = as.Dat
e("2015-01-05") -
        7, date.unit = "week")
p <- list()
p[["A"]] <- do.call(plot, c(common_plot_options, list(type = "obs", obs = "Incidence")))$trajec
tories +
    scale_y_continuous("Weekly incidence") + scale_x_date("", date_labels = "%b %Y")
p[["B"]] <- do.call(plot, c(common_plot_options, list(type = "obs", obs = "Serology")))$traject
ories +
    scale_y_continuous("Percent immune", labels = percent) + scale_x_date("",
    date_labels = "%b %Y")
p[["C"]] <- do.call(plot, c(common_plot_options, list(type = "state", state = "beta_track")))$t
rajectories +
    scale_y_continuous("Transmission rate") + scale_x_date("", date_labels = "%b %Y")
p[["D"]] <- do.call(plot, c(common_plot_options, list(type = "state", state = "Reff")))$traject
ories +
    scale_y_continuous("Reproduction number") + scale_x_date("", date_labels = "%b %Y")
plot <- do.call(plot_grid, c(p, list(labels = names(p), ncol = 2)))
plot
```


Weekly incidence
2000
1000
0
Jan 2015
Jul 2015
Jan 2016
Jul 2016
Percent immune
60%
40%
20%
0%
Jan 2015
Jul 2015
Jan 2016
Jul 2016
C
10.0
7.5
5.0
2.5
Transmission rate
D
3
2
1
Reproduction number



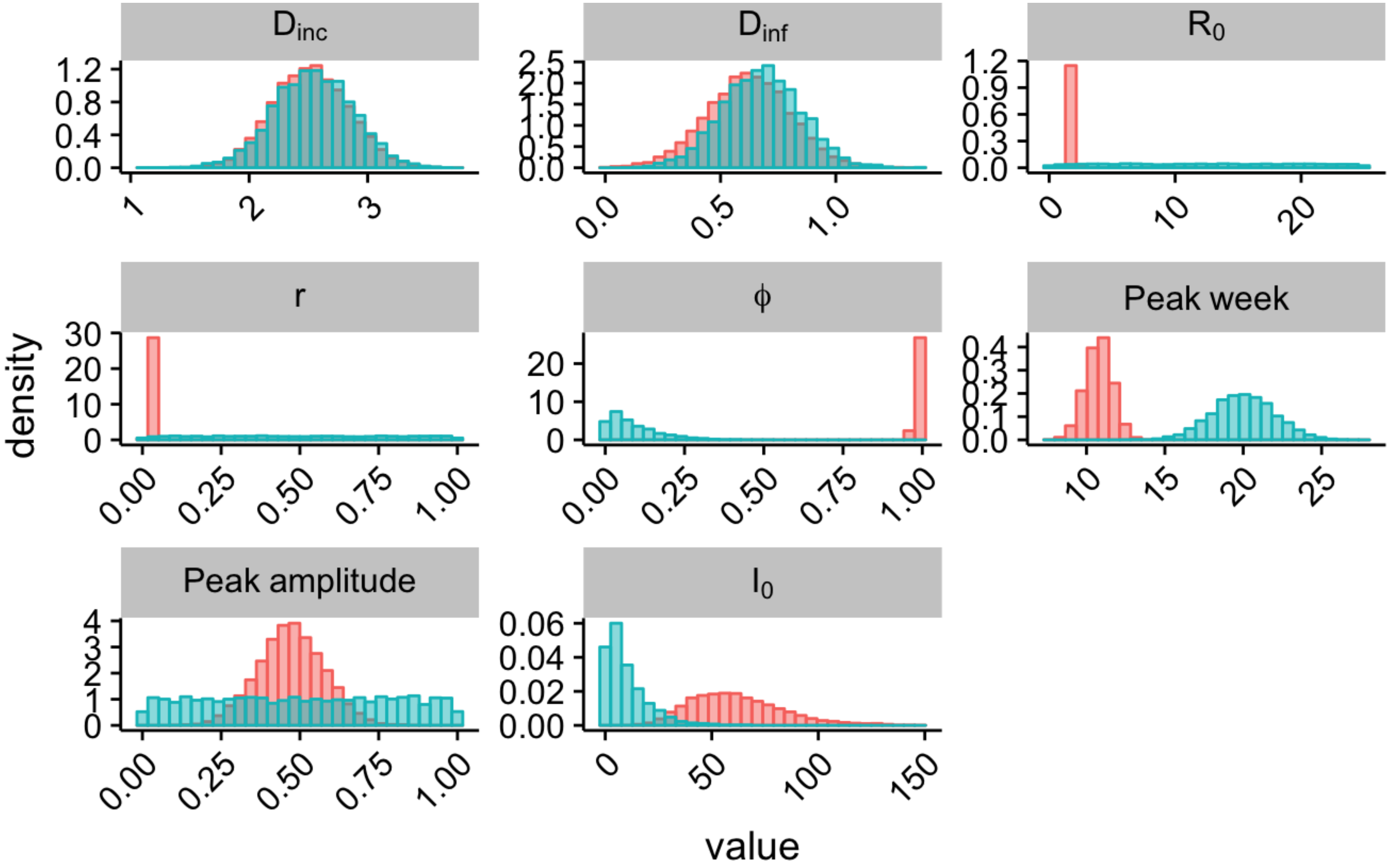
Parameter plots

\(D_\mathrm{inc}\): duration between mosquito infection caused by a human and subsequent human case to become infectious. \(D_\mathrm{inf}\): duration of human infectiousness. \(R_0\): basic reproduction number. \(r\): proportion of cases reported. \(\phi\): overdispersion of reporting. Peak week: Week of peak Zika transmission. Peak amplitude: Peak amplitude (as proportion of average transmission rate), \(I_0\): initial number of infectives.

```
p <- plot(pred, prior = bi_prior, type = c("param", "logeval"), labels = c(p_d_inc_h = "D[inc]"
,
    p_d_inf_h = "D[inf]", p_R0 = "R[0]", p_p_rep = "r", p_p_over = "phi", p_s_peak = "Peak~week
",
    p_s_amp = "Peak~amplitude", initI = "I[0]"), pairs = FALSE, plot = FALSE)
```

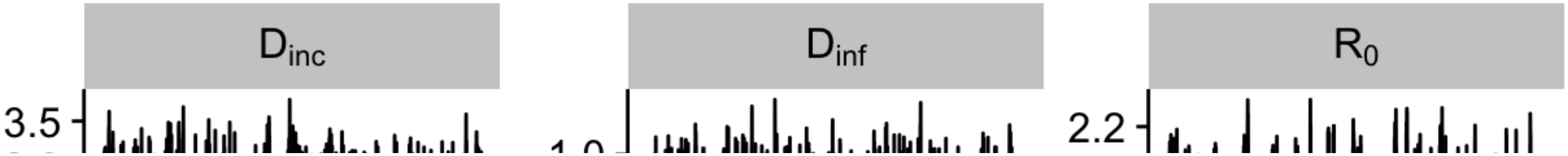
Plot parameter densities

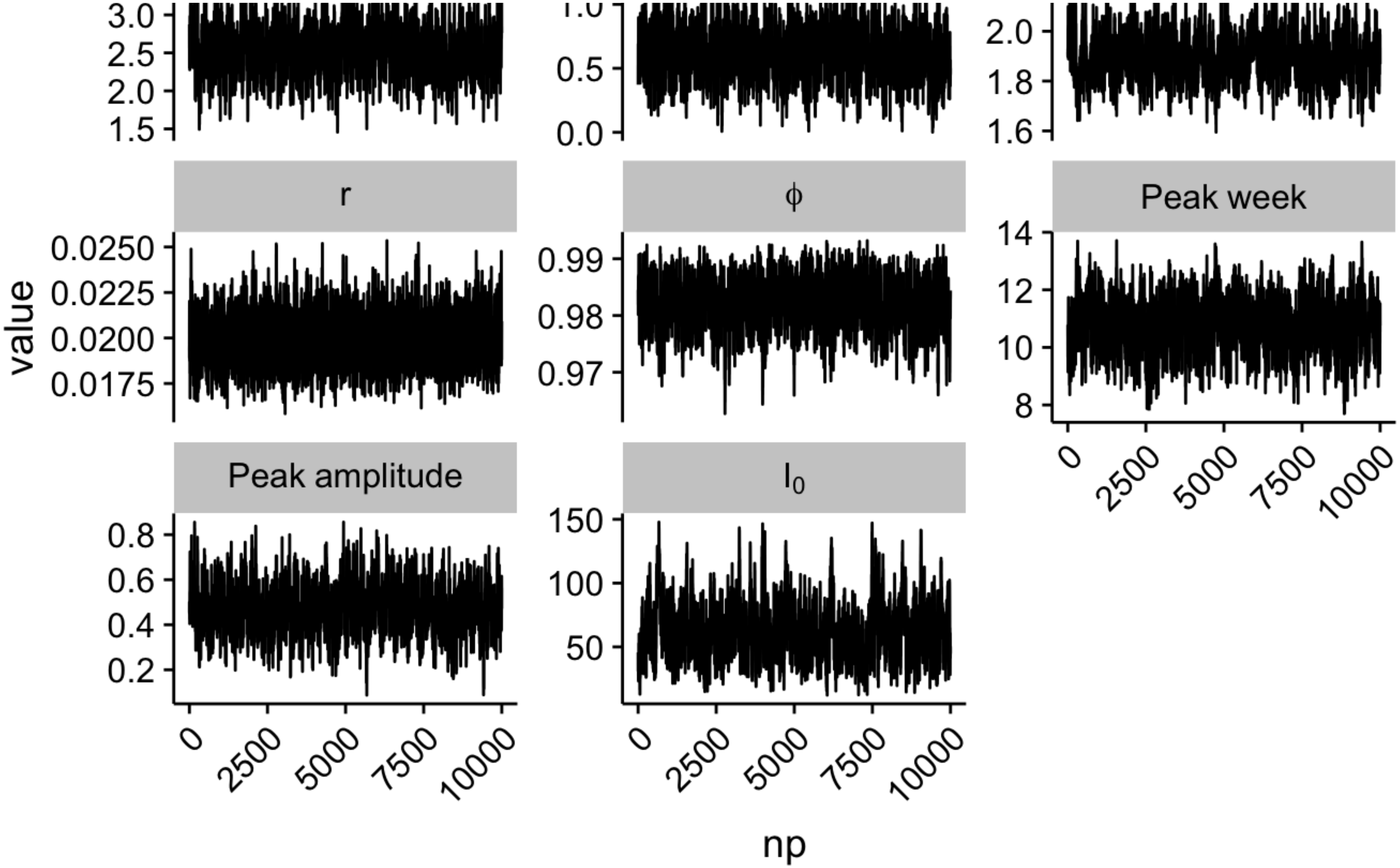
```
p$densities
```



Plot parameter traces

```
p$traces
```

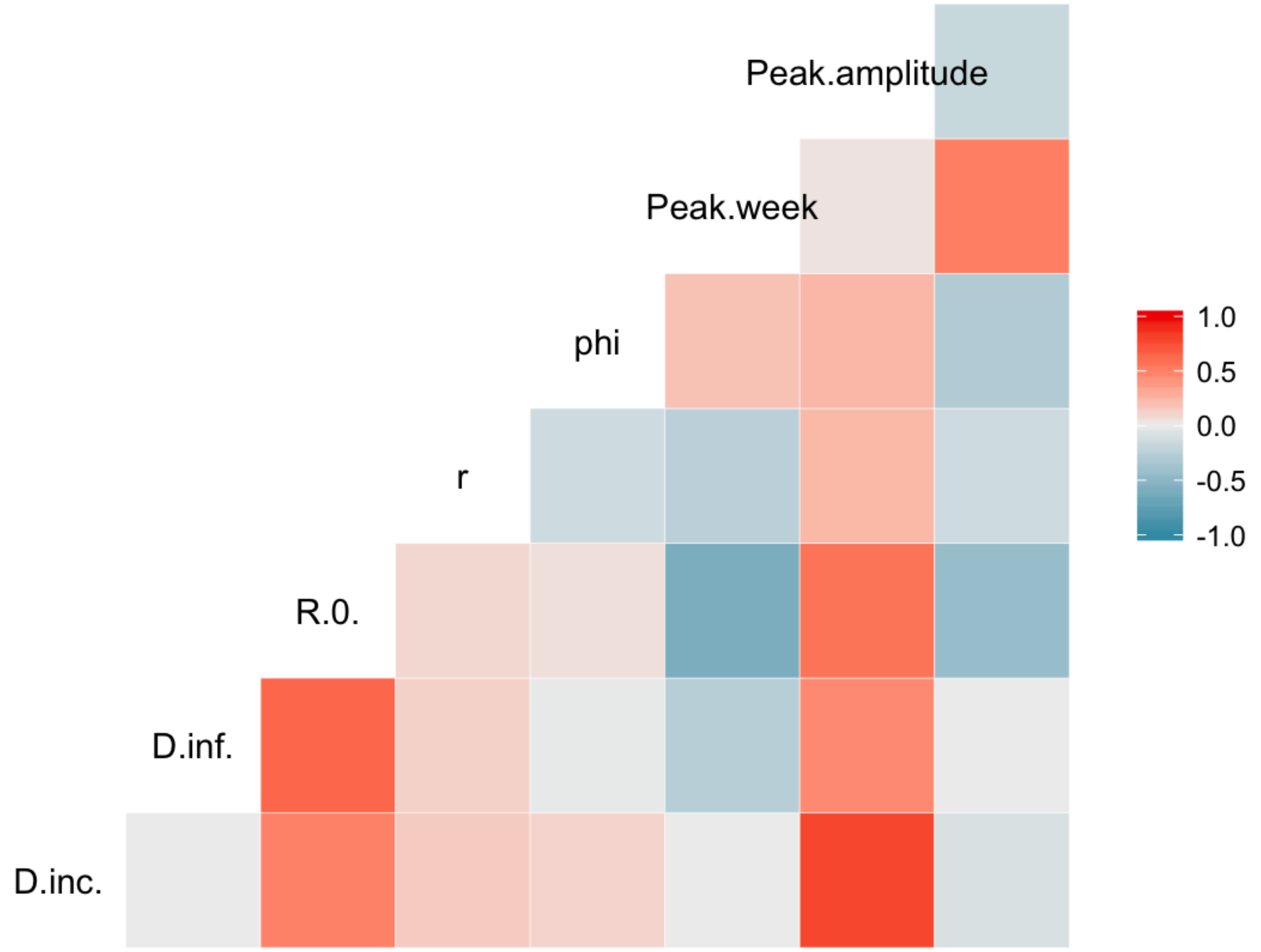




Plot paired correlations

```
p$correlations
```

I.0.



Session information

```r
sessionInfo()
```

```
## R version 3.4.1 (2017-06-30)
## Platform: x86_64-apple-darwin16.6.0 (64-bit)
## Running under: macOS Sierra 10.12.5
##
## Matrix products: default
## BLAS: /System/Library/Frameworks/Accelerate.framework/Versions/A/Frameworks/vecLib.framework
/Versions/A/libBLAS.dylib
## LAPACK: /System/Library/Frameworks/Accelerate.framework/Versions/A/Frameworks/vecLib.framewo
rk/Versions/A/libLAPACK.dylib
##
## locale:
## [1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices datasets  utils     methods   base
##
## other attached packages:
##  [1] bindrcpp_0.2      rbi.helpers_0.2   data.table_1.10.5
##  [4] rbi_0.8.0         dplyr_0.7.2       scales_0.4.1
##  [7] cowplot_0.7.0     ggplot2_2.2.1     magrittr_1.5
## [10] rmarkdown_1.5     Defaults_1.1-1
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.12.12       compiler_3.4.1     formatR_1.5
##  [4] RColorBrewer_1.1-2 plyr_1.8.4         bindr_0.1
##  [7] tools_3.4.1        ncdf4_1.16         digest_0.6.12
## [10] lubridate_1.6.0    evaluate_0.10      tibble_1.3.3
## [13] gtable_0.2.0       lattice_0.20-35    pkgconfig_2.0.1
## [16] rlang_0.1.1        GGally_1.3.2       yaml_2.1.14
## [19] coda_0.19-1        stringr_1.2.0      knitr_1.15.1
## [22] rprojroot_1.2      grid_3.4.1         reshape_0.8.6
## [25] glue_1.1.1         R6_2.2.2           reshape2_1.4.2
## [28] backports_1.0.5    codetools_0.2-15   htmltools_0.3.6
## [31] assertthat_0.2.0   colorspace_1.3-2   labeling_0.3
## [34] stringi_1.1.5      lazyeval_0.2.0     munsell_0.4.3
```